1642   1600

P#13

RAW SEQUENCE LISTING   DATE: 08/07/2002
PATENT APPLICATION: US/09/646,785A   TIME: 13:03:05

Input Set : A:\soei5042us.txt
Output Set: N:\CRF4\08072002\I646785A.raw

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 4 <110> APPLICANT: KISHIMOTO, Tadamitsu
 5        NAGASAWA, Takashi
 6        TACHIBANA, Kazunobu
 7        CHUGAI SEIYAKU KABUSIKI KAISHA
 9 <120> TITLE OF INVENTION: Vascularization Inhibitors
11 <130> FILE REFERENCE: 46124-5042-US
13 <140> CURRENT APPLICATION NUMBER: US 09/646,785A
14 <141> CURRENT FILING DATE: 2001-02-16
16 <150> PRIOR APPLICATION NUMBER: PCT/JP99/01448
17 <151> PRIOR FILING DATE: 1999-03-23
19 <150> PRIOR APPLICATION NUMBER: JP10/95448
20 <151> PRIOR FILING DATE: 1998-03-24
22 <160> NUMBER OF SEQ ID NOS: 12
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 352
26 <212> TYPE: PRT
27 <213> ORGANISM: Mus
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33             20                  25                  30
34 Glu Glu Asn Ala Asn Phe Asn Lys Ile Phe Leu Pro Thr Ile Tyr
35             35                  40                  45
36 Ser Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu Val Ile
37             50                  55                  60
38 Leu Val Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr Asp Lys
39             65                  70                  75
40 Tyr Arg Leu His Leu Ser Val Ala Asp Leu Leu Phe Val Ile Thr
41             80                  85                  90
42 Leu Pro Phe Trp Ala Val Asp Ala Val Ala Asn Trp Tyr Phe Gly
43             95                  100                 105
44 Asn Phe Leu Cys Lys Ala Val His Val Ile Tyr Thr Val Asn Leu
45             110                 115                 120
46 Tyr Ser Ser Val Leu Ile Leu Ala Phe Ile Ser Leu Asp Arg Tyr
47             125                 130                 135
48 Leu Ala Ile Val His Ala Thr Asn Ser Gln Arg Pro Arg Lys Leu
49             140                 145                 150
50 Leu Ala Glu Lys Val Val Tyr Val Gly Val Trp Ile Pro Ala Leu
51             155                 160                 165
52 Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asn Val Ser Glu Ala
53             170                 175                 180
54 Asp Asp Arg Tyr Ile Cys Asp Arg Phe Tyr Pro Asn Asp Leu Trp
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55                 185               190               195
56 Val Val Val Phe Gln Phe Gln His Ile Met Val Gly Leu Ile Leu
57                 200               205               210
58 Pro Gly Ile Val Ile Leu Ser Cys Tyr Cys Ile Ile Ile Ser Lys
59                 215               220               225
60 Leu Ser His Ser Lys Gly His Gln Lys Arg Lys Ala Leu Lys Thr
61                 230               235               240
62 Thr Val Ile Leu Ile Leu Ala Phe Phe Ala Cys Trp Leu Pro Tyr
63                 245               250               255
64 Tyr Ile Gly Ile Ser Ile Asp Ser Phe Ile Leu Leu Glu Ile Ile
65                 260               265               270
66 Lys Gln Gly Cys Glu Phe Glu Asn Thr Val His Lys Trp Ile Ser
67                 275               280               285
68 Ile Thr Glu Ala Leu Ala Phe Phe His Cys Cys Leu Asn Pro Ile
69                 290               295               300
70 Leu Tyr Ala Phe Leu Gly Ala Lys Phe Lys Thr Ser Ala Gln His
71                 305               310               315
72 Ala Leu Thr Ser Val Ser Arg Gly Ser Ser Leu Lys Ile Leu Ser
73                 320               325               330
74 Lys Gly Lys Arg Gly Gly His Ser Ser Val Ser Thr Glu Ser Glu
75                 335               340               345
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77                 350
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82 <212> TYPE: DNA
83 <213> ORGANISM: Mus
85 <220> FEATURE:
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87 <222> LOCATION: (1)...(1059)
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91 atg ggc tca ggg gac tat gac tcc atg aag gaa ccc tgt ttc cgt 90
92 gaa gaa aat gct aat ttc aat aaa atc ttc ctg ccc acc atc tac 135
93 tcc atc atc ttc tta act ggc att gtg ggc aat gga ttg gtc atc 180
94 ctg gtc atg ggt tac cag aag aaa ctg aga agc atg acg gac aag 225
95 tac agg ctg cac ctg tca gtg gcc gac ctc ctc ttt gtc atc acg 270
96 ctt ccc ttc tgg gca gtt gat gcc gtg gca aac tgg tac ttt ggg 315
97 aac ttc cta tgc aag gca gtc cat gtc atc tac aca gtc aac ctc 360
98 tac agc agt gtc ctc atc ctg gcc ttc atc agt ctg gac cgc tac 405
99 ctg gcc atc gtc cac gcc acc aac agt cag agg cca agg aag ctg 450
100 ttg gct gaa aag gtg gtc tat gtt ggc gtc tgg atc cct gcc ctc 495
101 ctg ctg act att ccc gac ttc atc ttt gcc aac gtc agt gag gca 540
102 gat gac aga tat atc tgt gac cgc ttc tac ccc aat gac ttg tgg 585
103 gtg gtt gtg ttc cag ttt cag cac atc atg gtt ggc ctt atc ctg 630
104 cct ggt att gtc atc ctg tcc tgc tat tgc att atc atc tcc aag 675
105 ctg tca cac tcc aag ggc cac cag aag cgc aag gcc ctc aag acc 720
106 aca gtc atc ctc atc ctg gct ttc ttc gcc tgt tgg ctg cct tac 765
107 tac att ggg atc agc atc gac tcc ttc atc ctc ctg gaa atc atc 810
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Input Set : A:\soei5042us.txt
Output Set: N:\CRF4\08072002\I646785A.raw

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108 aag caa ggg tgt gag ttt gag aac act gtg cac aag tgg att tcc 855
109 atc acc gag gcc cta gct ttc ttc cac tgt tgt ctg aac ccc atc 900
110 ctc tat gct ttc ctt gga gcc aaa ttt aaa acc tct gcc cag cac 945
111 gca ctc acc tct gtg agc aga ggg tcc agc ctc aag atc ctc tcc 990
112 aaa gga aag cga ggt gga cat tca tct gtt tcc act gag tct gag 1035
113 tct tca agt ttt cac tcc agc taa cacagatgta aaagactttt ttttat 1085
114 acgataaata acttttttt aagttacaca tttttcagat ataaaagact gaccaatatt 1145
115 gtacagtttt tattgcttgt tggatttttg tcttgtgttt ctttagtttt tgtgaagttt 1205
116 aattgactta tttatataaa ttttttttgt ttcatattga tgtgtgtcta ggcaggacct 1265
117 gtggccaagt tcttagttgc tgtatgtctc gtggtaggac tgtagaaaag ggaactgaac 1325
118 attccagagc gtgtagttaa tcacgtaaag ctagaaatga tccccagctg tttatgcata 1385
119 gataatctct ccattcccgt ggaacgtttt tcctgttctt aagacgtgat tttgctgtag 1445
120 aagatggcac ttataaccaa agcccaaagt ggtatagaaa tgctggtttt tcagttttca 1505
121 ggagtgggtt gatttcagca cctacagtgt acagtcttgt attaagttgt taataaaagt 1565
122 acatgttaaa cttaaaaaaa aaa                                    1588
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127 <212> TYPE: PRT
128 <213> ORGANISM: Mus

130 <400> SEQUENCE: 3

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133 Glu Glu Val Gly Ser Gly Asp Tyr Asp Ser Asn Lys Glu Pro Cys
134                  20                  25                  30
135 Phe Arg Asp Glu Asn Val His Phe Asn Arg Ile Phe Leu Pro Thr
136                  35                  40                  45
137 Ile Tyr Phe Ile Ile Phe Leu Thr Gly Ile Val Gly Asn Gly Leu
138                  50                  55                  60
139 Val Ile Leu Val Met Gly Tyr Gln Lys Lys Leu Arg Ser Met Thr
140                  65                  70                  75
141 Asp Lys Tyr Arg Leu His Leu Ser Val Ala Asp Leu Leu Phe Val
142                  80                  85                  90
143 Ile Thr Leu Pro Phe Trp Ala Val Asp Ala Met Ala Asp Trp Tyr
144                  95                 100                 105
145 Phe Gly Lys Phe Leu Cys Lys Ala Val His Ile Ile Tyr Thr Val
146                 110                 115                 120
147 Asn Leu Tyr Ser Ser Val Leu Ile Leu Ala Phe Ile Ser Leu Asp
148                 125                 130                 135
149 Arg Tyr Leu Ala Ile Val His Ala Thr Asn Ser Gln Arg Pro Arg
150                 140                 145                 150
151 Lys Leu Leu Ala Glu Lys Ala Val Tyr Val Gly Val Trp Ile Pro
152                 155                 160                 165
153 Ala Leu Leu Leu Thr Ile Pro Asp Phe Ile Phe Ala Asp Val Ser
154                 170                 175                 180
155 Gln Gly Asp Ile Ser Gln Gly Asp Asp Arg Tyr Ile Cys Asp Arg
156                 185                 190                 195
157 Leu Tyr Pro Asp Ser Leu Trp Met Val Val Phe Gln Phe Gln His
158                 200                 205                 210
159 Ile Met Val Gly Leu Ile Leu Pro Gly Ile Val Ile Leu Ser Cys
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160                215                220                225
161 Tyr Cys Ile Ile Ile Ser Lys Leu Ser His Ser Lys Gly His Gln
162                230                235                240
163 Lys Arg Lys Ala Leu Lys Thr Thr Val Ile Leu Ile Leu Ala Phe
164                245                250                255
165 Phe Ala Cys Trp Leu Pro Tyr Tyr Val Gly Ile Ser Ile Asp Ser
166                260                265                270
167 Phe Ile Leu Leu Gly Val Ile Lys Gln Gly Cys Asp Phe Glu Ser
168                275                280                285
169 Ile Val His Lys Trp Ile Ser Ile Thr Glu Ala Leu Ala Phe Phe
170                290                295                300
171 His Cys Cys Leu Asn Pro Ile Leu Tyr Ala Phe Leu Gly Ala Lys
172                305                310                315
173 Phe Lys Ser Ser Ala Gln His Ala Leu Asn Ser Met Ser Arg Gly
174                320                325                330
175 Ser Ser Leu Lys Ile Leu Ser Lys Gly Lys Arg Gly Gly His Ser
176                335                340                345
177 Ser Val Ser Thr Glu Ser Glu Ser Ser Ser Phe His Ser Ser
178                350                355
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182 <211> LENGTH: 1758
183 <212> TYPE: DNA
184 <213> ORGANISM: Mus
186 <220> FEATURE:
187 <221> NAME/KEY: CDS
188 <222> LOCATION: (1)...(1080)
189 <223> OTHER INFORMATION:
191 <400> SEQUENCE: 4
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193 gaa gaa gtg ggg tct gga gac tat gac tcc aac aag gaa ccc tgc 90
194 ttc cgg gat gaa aac gtc cat ttc aat agg atc ttc ctg ccc acc 135
195 atc tac ttc atc atc ttc ttg act ggc ata gtc ggc aat gga ttg 180
196 gtg atc ctg gtc atg ggt tac cag aag aag cta agg agc atg acg 225
197 gac aag tac cgg ctg cac ctg tca gtg gct gac ctc ctc ttt gtc 270
198 atc aca ctc ccc ttc tgg gca gtt gat gcc atg gct gac tgg tac 315
199 ttt ggg aaa ttt ttg tgt aag gct gtc cat atc atc tac act gtc 360
200 aac ctc tac agc agc gtt ctc atc ctg gcc ttc atc agc ctg gac 405
201 cgg tac ctc gcc att gtc cac gcc acc aac agt caa agg cca agg 450
202 aaa ctg ctg gct gaa aag gca gtc tat gtg ggc gtc tgg atc cca 495
203 gcc ctc ctc ctg act ata cct gac ttc atc ttt gcc gac gtc agc 540
204 cag ggg gac atc agt cag ggg gat gac agg tac atc tgt gac cgc 585
205 ctt tac ccc gat agc ctg tgg atg gtg gtg ttt caa ttc cag cat 630
206 ata atg gtg ggt ctc atc ctg ccc ggc atc gtc atc ctc tcc tgt 675
207 tac tgc atc atc atc tct aag ctg tca cac tcc aag ggc cac cag 720
208 aag cgc aag gcc ctc aag acg aca gtc atc ctc atc cta gct ttc 765
209 ttt gcc tgc tgg ctg cca tat tat gtg ggg atc agc atc gac tcc 810
210 ttc atc ctt ttg gga gtc atc aag caa gga tgt gac ttc gag agc 855
211 att gtg cac aag tgg atc tcc atc aca gag gcc ctc gcc ttc ttc 900
212 cac tgt tgc ctg aac ccc atc ctc tat gcc ttc ctc ggg gcc aag 945
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213 ttc aaa agc tct gcc cag cat gca ctc aac tcc atg agc aga ggc 990
214 tcc agc ctc aag atc ctt tcc aaa gga aag cgg ggt gga cac tct 1035
215 tcc gtc tcc acg gag tca gaa tcc tcc agt ttt cac tcc agc taa 1080
216 cccttatgca aagacttata taatatatat atatatatga taaagaactt ttttatgtta 1140
217 cacattttcc agatataaga gactgaccag tcttgtacag ttttttttttt ttttaattg 1200
218 actgttggga gtttatgttc ctctagtttt tgtgaggttt gacttaattt atataaatat 1260
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220 tagctgttta tctgtgtgta ggactgtaga actgtagagg aagaaactga acattccaga 1380
221 atgtgtggta aattgaataa agctagccgt gatcctcagc tgttgctgca taatctcttc 1440
222 attccgagga gcaccccacc cccaccccca ccccacccc attcttaaat tgtttggtta 1500
223 tgctgtgtga tggtttgttt ggttttttttt tgttgttgtt gttgttttt ttttctgtaa 1560
224 aagatggcac ttaaaaccaa agcctgaaat ggtggtagaa atgctggggt ttttttttgtt 1620
225 tgtttgtttt ttcagtttttc aagagtagat tgacttcagt ccctacaaat gtacagtctt 1680
226 gtattacatt gttaataaaa gtcaatgata aacttaaaaa aaaaaaaaaa aaaaaaaaa 1740
227 aaaaaaaaaa aaaaaaaa                                          1758
230 <210> SEQ ID NO: 5
231 <211> LENGTH: 89
232 <212> TYPE: PRT
233 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <223> OTHER INFORMATION: Ligand peptide
238 <400> SEQUENCE: 5
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243 Pro Cys Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys
244                35                40                  45
245 His Leu Lys Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val
246                50                55                  60
247 Ala Arg Leu Lys Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys
248                65                70                  75
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250                80                85
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254 <211> LENGTH: 2244
255 <212> TYPE: DNA
256 <213> ORGANISM: Mus
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260 <222> LOCATION: (471)...(743)
262 <400> SEQUENCE: 6
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265 ggaggcacgg ggcctggagg cgccaggcgg aggatgcggg cgacacggtg gcggcggcga 180
266 ccgcgcgacc gggcgggcgg gcgggcaggg gcgagcggag ggagggagcg gactgcggca 240
267 ggatctgtcg aggaaaaatc ttgcggccgg cgattccccg ccttttaagc gcagcctgca 300
268 ctccccccac cccacgcagg ggcgggcctt ccccaacgcg ggcgcccact ggccgccgcg 360
269 cgccgctccc ctccagctcg cctgcgcctc tcactctccg tcagccgcat tgcccgctcg 420
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/646,785A

DATE: 08/07/2002
TIME: 13:03:06

Input Set : **A:\soei5042us.txt**
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